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## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/077,040

DATE: 03/01/2002

TIME: 12:43:17

Input Set : N:\Crf3\RULE60\10077040.raw  
 Output Set: N:\CRF3\03012002\J077040.raw

## SEQUENCE LISTING

## 3 (1) GENERAL INFORMATION:

- 5 (i) APPLICANT: Lal, Preeti  
   Corley, Neil C.  
   Patterson, Chandra
- 9 (ii) TITLE OF INVENTION: HUMAN NEUROSECRETORY PROTEINS
- 11 (iii) NUMBER OF SEQUENCES: 6
- 13 (iv) CORRESPONDENCE ADDRESS:
  - 14   (A) ADDRESSEE: Incyte Pharmaceuticals, Inc.
  - 15   (B) STREET: 3174 Porter Dr.
  - 16   (C) CITY: Palo Alto
  - 17   (D) STATE: CA
  - 18   (E) COUNTRY: USA
  - 19   (F) ZIP: 94304
- 21 (v) COMPUTER READABLE FORM:
  - 22   (A) MEDIUM TYPE: Diskette
  - 23   (B) COMPUTER: IBM Compatible
  - 24   (C) OPERATING SYSTEM: DOS
  - 25   (D) SOFTWARE: FastSEQ for Windows Version 2.0
- 27 (vi) CURRENT APPLICATION DATA:
  - 28   (A) APPLICATION NUMBER: US/10/077,040
  - 29   (B) FILING DATE: 14-Feb-2002
  - 30   (C) CLASSIFICATION:
- 32 (vii) PRIOR APPLICATION DATA:
  - 33   (A) APPLICATION NUMBER: 09/062,601
  - 34   (B) FILING DATE:
- 37 (viii) ATTORNEY/AGENT INFORMATION:
  - 38   (A) NAME: Cerrone, Michael C.
  - 39   (B) REGISTRATION NUMBER: 39,132
  - 40   (C) REFERENCE/DOCKET NUMBER: PF-0510 US
- 42 (ix) TELECOMMUNICATION INFORMATION:
  - 43   (A) TELEPHONE: 650-855-0555
  - 44   (B) TELEFAX: 650-845-4166
  - 45   (C) TELEX:
- 48 (2) INFORMATION FOR SEQ ID NO: 1:
  - 50 (i) SEQUENCE CHARACTERISTICS:
    - 51   (A) LENGTH: 468 amino acids
    - 52   (B) TYPE: amino acid
    - 53   (C) STRANDEDNESS: single
    - 54   (D) TOPOLOGY: linear
  - 56 (vii) IMMEDIATE SOURCE:
    - 57   (A) LIBRARY: ISLTNOT01
    - 58   (B) CLONE: 2379427

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60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
 62 Met Gly Phe Leu Gly Thr Gly Thr Trp Ile Leu Val Leu Val Leu Pro  
 63 1 5 10 15  
 64 Ile Gln Ala Phe Pro Lys Pro Gly Gly Ser Gln Asp Lys Ser Leu His  
 65 20 25 30  
 66 Asn Arg Glu Leu Ser Ala Glu Arg Pro Leu Asn Glu Gln Ile Ala Glu  
 67 35 40 45  
 68 Ala Glu Glu Asp Lys Ile Lys Lys Thr Tyr Pro Pro Glu Asn Lys Pro  
 69 50 55 60  
 70 Gly Gln Ser Asn Tyr Ser Phe Val Asp Asn Leu Asn Leu Leu Lys Ala  
 71 65 70 75 80  
 72 Ile Thr Glu Lys Glu Lys Ile Glu Lys Glu Arg Gln Ser Ile Arg Ser  
 73 85 90 95  
 74 Ser Pro Leu Asp Asn Lys Leu Asn Val Glu Asp Val Asp Ser Thr Lys  
 75 100 105 110  
 76 Asn Arg Lys Leu Ile Asp Asp Tyr Asp Ser Thr Lys Ser Gly Leu Asp  
 77 115 120 125  
 78 His Lys Phe Gln Asp Asp Pro Asp Gly Leu His Gln Leu Asp Gly Thr  
 79 130 135 140  
 80 Pro Leu Thr Ala Glu Asp Ile Val His Lys Ile Ala Ala Arg Ile Tyr  
 81 145 150 155 160  
 82 Glu Glu Asn Asp Arg Ala Val Phe Asp Lys Ile Val Ser Lys Leu Leu  
 83 165 170 175  
 84 Asn Leu Gly Leu Ile Thr Glu Ser Gln Ala His Thr Leu Glu Asp Glu  
 85 180 185 190  
 86 Val Ala Glu Val Leu Gln Lys Leu Ile Ser Lys Glu Ala Asn Asn Tyr  
 87 195 200 205  
 88 Glu Glu Asp Pro Asn Lys Pro Thr Ser Trp Thr Glu Asn Gln Ala Gly  
 89 210 215 220  
 90 Lys Ile Pro Glu Lys Val Thr Pro Met Ala Ala Ile Gln Asp Gly Leu  
 91 225 230 235 240  
 92 Ala Lys Gly Glu Asn Asp Glu Thr Val Ser Asn Thr Leu Thr Leu Thr  
 93 245 250 255  
 94 Asn Gly Leu Glu Arg Arg Thr Lys Thr Tyr Ser Glu Asp Asn Phe Glu  
 95 260 265 270  
 96 Glu Leu Gln Tyr Phe Pro Asn Phe Tyr Ala Leu Leu Lys Ser Ile Asp  
 97 275 280 285  
 98 Ser Glu Lys Glu Ala Lys Glu Lys Glu Thr Leu Ile Thr Ile Met Lys  
 99 290 295 300  
 100 Thr Leu Ile Asp Phe Val Lys Met Met Val Lys Tyr Gly Thr Ile Ser  
 101 305 310 315 320  
 102 Pro Glu Glu Gly Val Ser Tyr Leu Glu Asn Leu Asp Glu Met Ile Ala  
 103 325 330 335  
 104 Leu Gln Thr Lys Asn Lys Leu Glu Lys Asn Ala Thr Asp Asn Ile Ser  
 105 340 345 350  
 106 Lys Leu Phe Pro Ala Pro Ser Glu Lys Ser His Glu Glu Thr Asp Ser  
 107 355 360 365  
 108 Thr Lys Glu Glu Ala Ala Lys Met Glu Lys Glu Tyr Gly Ser Leu Lys  
 109 370 375 380

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110 Asp Ser Thr Lys Asp Asn Ser Asn Pro Gly Gly Lys Thr Asp Glu  
111 385 390 395 400  
112 Pro Lys Gly Lys Thr Glu Ala Tyr Leu Ala Ile Arg Lys Asn Ile  
113 405 410 415  
114 Glu Trp Leu Lys Lys His Asp Lys Lys Gly Asn Lys Glu Asp Tyr Asp  
115 420 425 430  
116 Leu Ser Lys Met Arg Asp Phe Ile Asn Lys Gln Ala Asp Ala Tyr Val  
117 435 440 445  
118 Glu Lys Gly Ile Leu Asp Lys Glu Glu Ala Glu Ala Ile Lys Arg Ile  
119 450 455 460  
120 Tyr Ser Ser Leu  
121 465

123 (2) INFORMATION FOR SEQ ID NO: 2:

125 (i) SEQUENCE CHARACTERISTICS:  
126 (A) LENGTH: 1844 base pairs  
127 (B) TYPE: nucleic acid  
128 (C) STRANDEDNESS: single  
129 (D) TOPOLOGY: linear  
131 (vii) IMMEDIATE SOURCE:  
132 (A) LIBRARY: ISLTNOT01  
133 (B) CLONE: 2379427

135 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
137 CAGCGCTCCC CTCTACCTGG AGACTTGACT CCCCGCGCGCC CCAACCCTGC TTATCCCTG 60  
138 ACCGTCGAGT GTCAGAGATC CTGCAGCCGC CCAGTCCCGG CCCCTCTCCC GCCCCACACC 120  
139 CACCCCTCCTG GCTCTTCCTG TTTTACTCC TCCTTTCAT TCATAACAAA AGCTACAGCT 180  
140 CCAGGAGCCC AGCGCCGGGC TGTGACCCAA GCGGAGCGTG GAAGAATGGG GTTCCTCGGG 240  
141 ACCGGCACTT GGATTCTGGT GTTAGTGCTC CCGATTCAAG CTTTCCCCAA ACCTGGAGGA 300  
142 AGCCAAGACA AATCTCTACA TAATAGAGAA TTAAGTGCAG AAAGACCTT GAATGAACAG 360  
143 ATTGCTGAAG CAGAAGAAGA CAAGATTAAA AAAACATATC CTCCAGAAAA CAAGCCAGGT 420  
144 CAGAGCAACT ATTCTTTGT TGATAACTTG AACCTGCTAA AGGCAATAAC AGAAAAGGAA 480  
145 AAAATTGAGA AAGAAAGACA ATCTATAAGA AGCTCCAC TTGATAATAA GTTGAATGTG 540  
146 GAAGATGTTG ATTCAACCAA GAATCGAAAA CTGATCGATG ATTATGACTC TACTAAGAGT 600  
147 GGATTGGATC ATAAATTCA AGATGATCCA GATGGTCTTC ATCAACTAGA CGGGACTCCT 660  
148 TTAACCGCTG AAGACATTGT CCATAAAATC GCTGCCAGGA TTTATGAAGA AAATGACAGA 720  
149 GCCGTGTTG ACAAGATTGT TTCTAAACTA CTTAATCTCG GCCTTATCAC AGAAAGCCAA 780  
150 GCACATACAC TGGAAAGATGA AGTAGCAGAG GTTTTACAAA AATTAATCTC AAAGGAAGCC 840  
151 AACAAATTATG AGGAGGATCC CAATAAGCCC ACAAGCTGGA CTGAGAATCA GGCTGGAAAA 900  
152 ATACCAGAGA AAGTGAETCC AATGGCAGCA ATTCAAGATG GTCTTGCTAA GGGAGAAAAC 960  
153 GATGAAACAG TATCTAACAC ATTAACCTTG ACAAAATGGCT TGGAAAGGAG AACTAAAACC 1020  
154 TACAGTGAAG ACAACTTGA GGAACTCCAA TATTTCCTAA ATTCTATGC GCTACTGAAA 1080  
155 AGTATTGATT CAGAAAAAGA AGCAAAAGAG AAAGAAACAC TGATTACTAT CATGAAAACA 1140  
156 CTGATTGACT TTGTGAAGAT GATGGTGAAGA TATGGAACAA TATCTCCAGA AGAAGGTGTT 1200  
157 TCCTACCTTG AAAACTTGGA TGAAATGATT GCTCTTCAGA CCAAAAACAA GCTAGAAAAAA 1260  
158 AATGCTACTG ACAATATAAG CAAGCTTTTC CCAGCACCCT CAGAGAAGAG TCATGAAGAA 1320  
159 ACAGACAGTA CCAAGGAAGA AGCAGCTAAG ATGGAAAAGG AATATGGAAG CTTGAAGGAT 1380  
160 TCCACAAAAG ATGATAACTC CAACCCAGGA GGAAAGACAG ATGAACCCAA AGGAAAAACA 1440  
161 GAAGCCTATT TGGAAAGCCAT CAGAAAAAAAT ATTGAATGGT TGAAGAAACA TGACAAAAAG 1500  
162 GGAAATAAAG AAGATTATGA CCTTCAAAG ATGAGAGACT TCATCAATAA ACAAGCTGAT 1560  
163 GCTTATGTGG AGAAAGGCAT CCTTGACAAG GAAGAAGCCG AGGCCATCAA GGGCATTAT 1620

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164	AGCAGCCTGT	AAAAATGGCA	AAAGATCCAG	GAGTCTTCAG	ACTGTTTCAG	AAAACATAAT	1680
165	ATAGCTTAAA	ACACTTCTAA	TTCTGTGATT	AAAATTTTTT	GACCCAAGGG	TTATTAGAAA	1740
166	GTGCTGAATT	TACAGTAGTT	AACCTTTAC	AAGTGGTTAA	AACATAGCTT	TCTTCCCGTA	1800
167	AAAACATCT	GAAAGTAAAG	TTGTATGTAA	GCTGAAAAAA	AAAA		1844
169	(2) INFORMATION FOR SEQ ID NO: 3:						
171	(i) SEQUENCE CHARACTERISTICS:						
172	(A) LENGTH: 153 amino acids						
173	(B) TYPE: amino acid						
174	(C) STRANDEDNESS: single						
175	(D) TOPOLOGY: linear						
177	(vii) IMMEDIATE SOURCE:						
178	(A) LIBRARY: BRSTTUT14						
179	(B) CLONE: 2744187						
181	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:						
183	Met Ala Ala Gly Leu Phe Gly Leu Ser Ala Arg Arg	Leu Leu Ala Ala					
184	1	5	10	15			
185	Ala Ala Thr Arg Gly Leu Pro Ala Ala Arg Val Arg	Trp Glu Ser Ser					
186	20	25	30				
187	Phe Ser Arg Thr Val Val Ala Pro Ser Ala Val Ala	Gly Lys Arg Pro					
188	35	40	45				
189	Pro Glu Pro Thr Thr Pro Trp Gln Glu Asp Pro	Glu Pro Glu Asp Glu					
190	50	55	60				
191	Asn Leu Tyr Glu Lys Asn Pro Asp Ser His	Gly Tyr Asp Lys Asp Pro					
192	65	70	75	80			
193	Val Leu Asp Val Trp Asn Met Arg Leu Val Phe	Phe Gly Val Ser					
194	85	90	95				
195	Ile Ile Leu Val Leu Gly Ser Thr Phe Val Ala	Tyr Leu Pro Asp Tyr					
196	100	105	110				
197	Arg Met Lys Glu Trp Ser Arg Arg Glu Ala Glu Arg	Leu Val Lys Tyr					
198	115	120	125				
199	Arg Glu Ala Asn Gly Leu Pro Ile Met Glu Ser Asn	Cys Phe Asp Pro					
200	130	135	140				
201	Ser Lys Ile Gln Leu Pro Glu Asp Glu						
202	145	150					
204	(2) INFORMATION FOR SEQ ID NO: 4:						
206	(i) SEQUENCE CHARACTERISTICS:						
207	(A) LENGTH: 1463 base pairs						
208	(B) TYPE: nucleic acid						
209	(C) STRANDEDNESS: single						
210	(D) TOPOLOGY: linear						
212	(vii) IMMEDIATE SOURCE:						
213	(A) LIBRARY: BRSTTUT14						
214	(B) CLONE: 2744187						
216	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:						
218	CAGCCGCTGG	CTCCGTTCA	CTTCCCAGCC	ACCCCCGCTG	CTGCTACCAT	GATCTGCCAG	60
219	CCTGGGTGAT	GCTTCCTGCA	GGGACTCTTC	TCGGCCCGGG	CTGTCAGGA	AGGGCTCCCA	120
220	GACATCACCT	CTGCCCGCCG	CCACCTCCTC	CAACTCTCCC	AGCTCAGCCG	GAGCCGGAGC	180
221	GCGCAACAAAC	CAAGTCCGAG	ACTGGAGGCA	GATCGGGGGG	AGGGGAGAAG	CGCCAAGCGC	240
222	GCTGCCCTCC	CAGGGAAACT	CACTGCCGCC	TACTCCCAGC	CGGCCACAGT	CACCAGCTCA	300

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223	AAATGGCGAC	GACCGAGAAGG	GAGTCGGCGC	TCCGACCACC	ATCCACCTAC	TAAGGAAGCG	360
224	CGCTCTGGCC	GGCCCCGGCG	ATTGGTCACC	GCCCCGCTAGG	GGACAGCCCT	GGCCTCCTCT	420
225	GATTGGCAAG	CGCTGGCCAC	CTCCCCACAC	CCCTTGCAGAA	CGCTCCCTA	GTGGAGAAAA	480
226	GGAGTAGCTA	TTAGCCAATT	CGGGCAGGGC	CCGCTTTTA	GAAGCTGAT	TTCTTTGAA	540
227	GATGAAAGAC	TAGCGGAAGC	TCTGCCTCTT	TCCCAGTGG	GCGAGGGAAC	TCGGGGCGAT	600
228	TGGCTGGAA	CTGTATCCAC	CAAATGTAC	CGATTCTTCC	TATGCAGGAA	ATGAGCAGAC	660
229	CCATCAATAA	GAAATTTCTC	AGCCTGCCG	AAAATGGTTG	GCCCCACGAA	GCCACGACAA	720
230	CTGGAGGCAA	AGAGGGTTGC	TCAACGCC	GCCTCATTGG	AAAACCAAAT	CAGATCTGGG	780
231	ACCTATATAG	CGTGGCGGAG	GCAGGGCGAT	GATTGTCGCG	CTCGCACCC	CTGCAGCTGC	840
232	GCACAGTCGC	ATTCTTTCC	CCGCCCCCTGA	GACCCCTGCAG	CACCATCTGT	CATGGCGGCT	900
233	GGGCTGTTTG	GTGGAGCGC	TCGCGTCTT	TTGGCGCAG	CGGCGACGCG	AGGGCTCCCG	960
234	GCCGCCCGCG	TCCGCTGGGA	ATCTAGCTTC	TCCAGGACTG	TGGTCGCC	GTCCGCTGTG	1020
235	GCGGGAAAGC	GGCCCCCAGA	ACCGACCACA	CCGTGGCAAG	AGGACCCAGA	ACCCGAGGAC	1080
236	GAAAACCTGT	ATGAGAAGAA	CCCAGACTCC	CATGGTTATG	ACAAGGACCC	CGTTTTGGAC	1140
237	GTCTGGAACA	TGCCACTTGT	CTTCTCTTT	GGCGTCTCCA	TCATCCTGGT	CCTTGGCAGC	1200
238	ACCTTGTGG	CCTATCTGCC	TGACTACAGG	ATGAAAGAGT	GGTCCCGCCG	CGAAGCTGAG	1260
239	AGGCTTGTGA	AATACCGAGA	GGCCAATGGC	CTTCCCATCA	TGGAATCCAA	CTGCTTCGAC	1320
240	CCCAGCAAGA	TCCAGCTGCC	AGAGGATGAG	TGACCCAGTTG	CTAAGTGGGG	CTCAAGAAGC	1380
241	ACCGCCTTCC	CCACCCCCCTG	CCTGCCATTC	TGACCTCTTC	TCAGAGCACC	TAATTAAAGG	1440
242	GGCTGAAAGT	CTGAAAAAAA	AAA				1463

244 (2) INFORMATION FOR SEQ ID NO: 5:

246 (i) SEQUENCE CHARACTERISTICS:  
 247 (A) LENGTH: 471 amino acids  
 248 (B) TYPE: amino acid  
 249 (C) STRANDEDNESS: single  
 250 (D) TOPOLOGY: linear

252 (vii) IMMEDIATE SOURCE:

253 (A) LIBRARY: GenBank  
 254 (B) CLONE: 413764

256 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

258	Met	Gly	Phe	Leu	Trp	Thr	Gly	Ser	Trp	Ile	Leu	Val	Leu	Val	Leu	Asn
259	1				5					10					15	
260	Ser	Gly	Pro	Ile	Gln	Ala	Phe	Pro	Lys	Pro	Glu	Gly	Ser	Gln	Asp	Lys
261					20				25					30		
262	Ser	Leu	His	Asn	Arg	Glu	Leu	Ser	Ala	Glu	Arg	Pro	Leu	Asn	Glu	Gln
263					35				40					45		
264	Ile	Ala	Glu	Ala	Glu	Ala	Asp	Lys	Ile	Lys	Lys	Ala	Phe	Pro	Ser	Glu
265					50				55					60		
266	Ser	Lys	Pro	Ser	Glu	Ser	Asn	Tyr	Ser	Ser	Val	Asp	Asn	Leu	Asn	Leu
267					65				70					75		80
268	Leu	Arg	Ala	Ile	Thr	Glu	Lys	Glu	Thr	Val	Glu	Lys	Glu	Arg	Gln	Ser
269					85				90					95		
270	Ile	Arg	Ser	Pro	Pro	Phe	Asp	Asn	Gln	Leu	Asn	Val	Glu	Asp	Ala	Asp
271					100				105					110		
272	Ser	Thr	Lys	Asn	Arg	Lys	Leu	Ile	Asp	Glu	Tyr	Asp	Ser	Thr	Lys	Ser
273					115				120					125		
274	Gly	Leu	Asp	His	Lys	Phe	Gln	Asp	Asp	Pro	Asp	Gly	Leu	His	Gln	Leu
275					130				135					140		
276	Asp	Gly	Thr	Pro	Leu	Thr	Ala	Glu	Asp	Ile	Val	His	Lys	Ile	Ala	Thr

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L:28 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:29 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]